SEQUENCE LISTING

<110> Susanne LEONHARTSBERGER

Thomas MAIER

<120> METHOD FOR FERMENTATIVE PREPARATION OF S-ADENOSYLMETHIONINE

<130> LEONHARTSBERGER ET AL. - 1

<140> German No. 103 09 856.9

<141> 03-06-2003

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 384

<212> PRT

<213> Escherichia coli

<400> 1

Met Ala Lys His Leu Phe Thr Ser Glu Ser Val Ser Glu Gly His Pro
1 5 10 15

Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu
20 25 30

Glu Gln Asp Pro Lys Ala Arg Val Ala Cys Glu Thr Tyr Val Lys Thr
35 40 45

Gly Met Val Leu Val Gly Gly Glu Ile Thr Thr Ser Ala Trp Val Asp
50 55 60

Ile Glu Glu Ile Thr Arg Asn Thr Val Arg Glu Ile Gly Tyr Val His
65 70 75 80

Ser Asp Met Gly Phe Asp Ala Asn Ser Cys Ala Val Leu Ser Ala Ile
85 90 95

Gly Lys Gln Ser Pro Asp Ile Asn Gln Gly Val Asp Arg Ala Asp Pro
100 105 110

Leu Glu Gln Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr
115 120 125

Asn Glu Thr Asp Val Leu Met Pro Ala Pro Ile Thr Tyr Ala His Arg
130 135 140

Leu Val Gln Arg Gln Ala Glu Val Arg Lys Asn Gly Thr Leu Pro Trp
145 150 155 160

Leu Arg Pro Asp Ala Lys Ser Gln Val Thr Phe Gln Tyr Asp Asp Gly
165 170 175

Lys Ile Val Gly Ile Asp Ala Val Val Leu Ser Thr Gln His Ser Glu
180 185 190

Glu Ile Asp Gln Lys Ser Leu Gln Glu Ala Val Met Glu Glu Ile Ile
195 200 205

Lys Pro Ile Leu Pro Ala Glu Trp Leu Thr Ser Ala Thr Lys Phe Phe
210 215 220

Ile Asn Pro Thr Gly Arg Phe Val Ile Gly Gly Pro Met Gly Asp Cys
225 230 235 240

Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala
245 250 255

Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp
260 265 270

Arg Ser Ala Ala Tyr Ala Ala Arg Tyr Val Ala Lys Asn Ile Val Ala
275 280 285

Ala Gly Leu Ala Asp Arg Cys Glu Ile Gln Val Ser Tyr Ala Ile Gly
290 295 300

Val Ala Glu Pro Thr Ser Ile Met Val Glu Thr Phe Gly Thr Glu Lys
305 310 315 320

Val Pro Ser Glu Gln Leu Thr Leu Leu Val Arg Glu Phe Phe Asp Leu
325 330 335

Arg Pro Tyr Gly Leu Ile Gln Met Leu Asp Leu Leu His Pro Ile Tyr
340 345 350

Lys Glu Thr Ala Ala Tyr Gly His Phe Gly Arg Glu His Phe Pro Trp
355 360 365

Glu Lys Thr Asp Lys Ala Gln Leu Leu Arg Asp Ala Ala Gly Leu Lys
370 375 380

<210> 2

<211> 1155

<212> DNA

<213> Escherichia coli

<220>

<221> gene

<222> (1)..(1152)

<223> metK

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<306> 1453-1474

<307> 1997

<400> 2

atggcaaaac acctttttac gtccgagtcc gtctctgaag ggcatcctga caaaattgct 60

gaccaaattt ctgatgccgt tttagacgcg atcctcgaac aggatccgaa agcacgcgtt 120

gcttgcgaaa cctacgtaaa aaccggcatg gttttagttg gcggcgaaat caccaccagc 180

gcctgggtag acatcgaaga gatcacccgt aacaccgttc gcgaaattgg ctatgtgcat 240

tccgacatgg gctttgacgc taactcctgt gcggttctga gcgctatcgg caaacagtct 300

cctgacatca accagggcgt tgaccgtgcc gatccgctgg aacagggcgc gggtgaccag 360

ggtctgatgt ttggctacgc aactaatgaa accgacgtgc tgatgccagc acctatcacc 420

tatgcacacc gtctggtaca gcgtcaggct gaagtgcgta aaaacggcac tctgccgtgg 480

ctgcgcccgg acgcgaaaag ccaggtgact tttcagtatg acgacggcaa aatcgttggt 540

atcgatgctg tcgtgctttc cactcagcac tctgaagaga tcgaccagaa atcgctgcaa 600

gaagcggtaa tggaagagat catcaagcca attctgcccg ctgaatggct gacttctgcc 660

accaaattct tcatcaaccc gaccggtcgt ttcgttatcg gtggcccaat gggtgactgc 720

ggtctgactg gtcgtaaaat tatcgttgat acctacggcg gcatggcgcg tcacggtggc 780

ggtgcattct ctggtaaaga tccatcaaaa gtggaccgtt ccgcagccta cgcagcacgt 840

tatgtcgcga aaaacatcgt tgctgctggc ctggccgatc gttgtgaaat tcaggtttcc 900

tacgcaatcg gcgtggctga accgacctcc atcatggtag aaactttcgg tactgagaaa 960

gtgccttctg aacaactgac cctgctggta cgtgagttct tcgacctgcg cccatacggt 1020

ctgattcaga tgctggatct gctgcacccg atctacaaag aaaccgcagc atacggtcac 1080

tttggtcgtg aacatttccc gtgggaaaaa accgacaaag cgcagctgct gcgcgatgct 1140

gccggtctga agtaa 1155

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide metK2

<400> 3

ccttaattaa tgtctgttgt ggttggtgt 29

<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide metK4

<400> 4

ggaattctct ttaggaggta ttaaatatg 29

<210> 5

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide RLSS1

<400> 5

ctagcaggag gaattcacca tgggacctgt ggatggc 37

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide RLSS2

<400> 6

gggtaccccg ctaaaacaca agcttcttgg ggacctccca 40

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide GAPDHfw

<400> 7

gtcgacgcgt gaggcgagtc agtcgcgtaa tgc 33

<210> 8

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide GAPDHrevII

<400> 8

gaccttaatt aagatctcat atattccacc agctatttgt tag 43

<210> 9

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Multiple Cloning Site

<400> 9

gaagatctag gaggcctagc atatgtgaat tcccgggctg cagctg 46

<210> 10

<211> 1185

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(1185)

<223> RLSS-Gen

<400> 10

atg gga cct gtg gat ggc ttg tgt gac cat tct cta agt gaa gag gga 48
Met Gly Pro Val Asp Gly Leu Cys Asp His Ser Leu Ser Glu Glu Gly
1 5 10 15

gcc ttc atg ttc aca tct gaa tcg gta gga gaa ggg cat cca gat aag 96
Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys
20 25 30

atc tgt gac cag att agt gat gca gtg ctg gat gcc cat ctc aag caa 144
Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln
35 40 45

gac ccc aat gcc aag gtg gcc tgt gag aca gtg tgc aag aca ggg atg 192
Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met
50 55 60

gtg ctc ctg tgt gga gag atc acc tca atg gcc atg att gac tac cag 240
Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln
65 70 75 80

cgg gtg gtg aga gac acc att aag cac att ggc tac gat gac tct gcc 288
Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala
85 90 95

aag ggc ttc gac ttc aag acc tgc aat gtg ctc gtg gct ctg gag caa 336
Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln
100 105 110

cag tcc cca gac att gcc caa tgt gtc cat cta gac aga aat gag gag 384
Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu
115 120 125

gac gtt ggt gca gga gat cag ggt ctg atg ttc ggc tat gcc act gac 432
Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp
130 135 140

gag aca gag gag tgc atg ccg ctc acc att gtt ctt gct cac aaa ctc 480
Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145 150 155 160

aac acc cgg atg gca gat ctg agg cgc tct ggt gtc ctt ccc tgg ctg 528
Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu
165 170 175

aga cct gat tct aag act cag gta aca gtt cag tac gtg cag gat aat 576
Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn
180 185 190

ggt gct gtc atc cct gtt cgc gtc cac acc atc gtc atc tct gtg caa 624
Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln
195 200 205

cac aac gaa gac ata aca ctg gag gcc atg cga gag gcc ctg aag gag 672
His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu
210 215 220

cag gtg atc aaa gct gtg gtg cca gcc aag tac ctg gat gaa gac acc 720
Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr
225 230 235 240

atc tac cac ctg cag cca agt ggg cgg ttt gtc atc gga ggt ccc cag 768
Ile Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln
245 250 255

ggg gat gca ggt gtc aca ggc cgc aag att att gtg gac aca tac gga 816
Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
260 265 270

ggc tgg ggt gcc cat ggt ggt ggt gcc ttc tct gga aag gac tac acc 864
Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr
275 280 285

aag gtg gac cgc tca gca gct tat gcc gcc cgc tgg gtg gcc aag tct 912
Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser
290 295 300

ctg gtg aag gct ggg ctc tgc cgg aga gtc ctt gtt cag gtg tcc tat 960
Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr
305 310 315 320

gcc att ggt gtg gca gaa cct ctg tcc att tcc att ttc acc tac gga 1008
Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly

325 330 335

act tcc aag aag acc gag cga gag cta cta gag gtt gtg aac aag aac 1056
Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn
340 345 350

ttt gac ctc cgg ccg ggt gtt att gtc agg gac ttg gat ctg aag aag 1104
Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys
355 360 365

ccc atc tac cag aag act gca tgc tat ggt cat ttc gga aga agc gag 1152
Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu
370 375 380

ttt ccc tgg gag gtc ccc aag aag ctt gtg ttt 1185
Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe
385 390 395

<210> 11

<211> 395

<212> PRT

<213> Rattus norvegicus

<400> 11

Met Gly Pro Val Asp Gly Leu Cys Asp His Ser Leu Ser Glu Glu Gly
1 5 10 15

Ala Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys
20 25 30

Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln
35 40 45

Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met

50 55 60

Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Ile Asp Tyr Gln

65 70 75 80

Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala

85 90 95

Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln

100 105 110

Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu

115 120 125

Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp

130 135 140

Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu Ala His Lys Leu

145 150 155 160

Asn Thr Arg Met Ala Asp Leu Arg Arg Ser Gly Val Leu Pro Trp Leu
165 170 175

Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Val Gln Asp Asn
180 185 190

Gly Ala Val Ile Pro Val Arg Val His Thr Ile Val Ile Ser Val Gln
195 200 205

His Asn Glu Asp Ile Thr Leu Glu Ala Met Arg Glu Ala Leu Lys Glu
210 215 220

Gln Val Ile Lys Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr
225 230 235 240

Ile Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln
245 250 255

Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
260 265 270

Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr
275 280 285

Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser
290 295 300

Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr
305 310 315 320

Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly
325 330 335

Thr Ser Lys Lys Thr Glu Arg Glu Leu Leu Glu Val Val Asn Lys Asn
340 345 350

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys
355 360 365

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu
370 375 380

Phe Pro Trp Glu Val Pro Lys Lys Leu Val Phe

385 390 395